DSP-3, encoded by 552 base pairs

1	CCCCGCCGCT	CCTCCTCCCT	GTAACATGCC	ATAGTGCGCC	TGCGACCACA	CGGCCGGGGC
61	GCTAGCGTTC	GCCTTCAGCC	ACCATG GGGA	ATGGGATGAA	CAAGATCCTG	CCCGGCCTGT
121	ACATCGGCAA	CTTCAAAGAT	GCCAGAGACG	CGGAACAATT	GAGCAAGAAC	AAGGTGACAC
181	ATATTCTGTC	TGTCCACGAT	AGTGCCAGGC	CTATGTTGGA	GGGAGTTAAA	TACCTGTGCA
241	TCCCAGCAGC	GGATTCACCA	TCTCAAAACC	TGACAAGACA	TTTCAAAGAA	AGTATTAAAT
301	TCATTCACGA	GTGCCGGCTC	CGCGGTGAGA	GCTGCCTTGT	ACACTGCCTG	GCCGGGGTCT
361	CCAGGAGCGT	GACACTGGTG	ATCGCATACA	TCATGACCGT	CACTGACTTT	GGCTGGGAGG
421	ATGCCCTGCA	CACCGTGCGT	GCTGGGAGAT	CCTGTGCCAA	CCCCAACGTG	GGCTTCCAGA
481	GACAGCTCCA	GGAGTTTGAG	AAGCATGAGG	TCCATCAGTA	TCGGCAGTGG	CTGAAGGAAG
541		GAGCCCTTTG				
601	GAATTCTGAA	GTTCTGGGCC	TTTCTCAGAA	GACTGTAATG	TACCTGAAGT	TTCTGAAATA
661	TTGCAAACCC	GCAGAGTTTA	GGCTGGTGCT	GCCAAAAAGA	AAAGCAACAT	AGAGTTTAAG
721		TGATTTGTAA				
781	TTTATGTTGA	GAACTAAGGA	TATTCTTTAG	CAAGAGAAAA	TATTTTCCCC	TTATCCCCAC
841	TGCTGTGGAG	GTTTCTGTAC	CTCGCTTGGA	TGCCTGTAAG	GATCCCGGGA	GCCTTGCCGC
901	ACTGCCTTGT	GGGTGGCTTG	GCGCTC	•		

Translated full length protein, 184 amino acids

MGNGMNKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLEGVKYLCIPAADSPS QNLTRHFKESIKFIHECRLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA GRSCANPNVGFQRQLQEFEKHEVHQYRQWLKEEYGESPLQDAEEAKNILAAPGILKFWAF LRRL*

FIG. 2

FIG. 3

FIG. 1	3		
PYSI1 MKP-7 hVII5 PIC1 MKP-1 MKP-4 MKP-4 MKP-5 VIR USP-3 Consensus		PYST1 HKP-7 hVII5 PRC1 HKP-4 HKP-4 HKP-5 VHR DSP-3 Consensus	
FPENISI IN LUXSIE IN LUXSIE IN LUXSIE IN LUXSIE IN FRENISI IN FRENIE IN FRENIE IN FRENIE IN FERNIE IN FERN		SULURD-PI ORELP GLCEGKT PHONLPT PLSTSVPI PVPPSNTI SERALISI SGSFELSVQI	1 10
I DEA-RGKMGAVI I DEA-RSKKGGV I DSV-KNSGGRV I DSV-KNGGRV I LUSI-KNOGGRV Y LUAV-KUCRGRV Y LUAV-KUCRGRV I LUGALAUKHGKV I LUGALAUKHGRV I LUGALAUKHGRV I LUGALAUKHGRV F LUGALAUKHGRV		ASOLIOSDIGSPI JCGKPVVHVS JCGKPVVHSS JCHLESGUSSCI JCHLESGUSSDI JCHLESGU	
ATANC 1 948484 ANT HATH ACTAINCHEABASBAILTAINATH ACTAINCHEABASBAILTAINATH ACTAINCHEABASBAILTCHUATH ACTAINCHEABASBAILTCHUATH ACTAINCHEABASBAILTCHUATH ACTAINCHEABASBAILTCHUATH ACTAINCHEABASBAILTCHUATH ACTAINCHEABASBAILTCHUATH ACTAINCHEABASBAILTCHUATH ACTAINCHEABASBAILTCHUATH ANTAINCHEABASBAILTAINATH ANTAINCHEABASBAILTAINTAINATH ANTAINCHEABASBAILTAINATH ANTAINCHEABASBAILTAINATH ANTAINCHEABASBAILTAINTAINTAINTAINTAINTAINTAINTAINTAINTAIN	130	E SHSOPSE PV. LSHSOPSE PV. LSHS	
FPENISI JDEN-RGKNUGVI, VIII. IBI SESVI VI VARI BIJKI BI, SHIDIYDI VKIKKSHI SI'HE HI 1690 I. DET RELGE SS FPENISI JDEN-RSKUGVI, VIII. IBI SESVI VI VIIVINI BIJKI BI, SURKI BI VKRKKSHI SI'HE HI 1690 I. DET RELGE SS LIKSIEL IDKH-KL SSCOVJVIII. IBI SESVI LELIAY LIKE HICHSSIDIYDE VKORREPS I. SI'HE HI 1690 I. DET RELGE SS LIKE I IDSV-KNSGGRVLVIICOBGI SESDI JULINYLJOSHRVAL DEBT EF VKORRSI I.SI'HE SI HGOL LOFE SOVI IN PHENIEY JDAV-KUCRGRVLVIICOBGI SESDI JULINYLJOKKRVAL DEBT EF VKORRSI I.SI'HE SI HGOL LOFE SOVI IN PHENIEY JDAV-KUCRGRVLVIICOBGI SESDI JULINYLJOKKRVAL EEN EF VKORRSI I.SI'HE SI HGOL LOFE SOVI IN PHENIEY JDAV-KOR I DET SOVI IN PHENIEY JDAV-KORRSI I.SI'HE SI HGOL COLNIRLOKE GERNODT JOROKAGRVLVIICOBGSSESPI JULINYLJOHRAKROVERI SI VKORRSI VI VROBRSIVSI I GROL OFFEKNIEVIJOYROKSI SI VROBRE JORNOVER GROL OFFEKNIEVIJOYRO FKESIKF IHEC-RLRGESCLVIICLOGVSRSVI LVIITYLJOHRAKROVKSOL SI VROGRSCOMUNVGI GROL OFFEKNIEVIJOYRO VLVIICLOGVSRSVI LVIITYLJOHRAKROVKSOL SI VROGRSCOMUNVGI GROL OFFEKNIEVIJOYRO VLVI KARAKROVA VLVIICLOGVSRSVI LVIJAYLJOHRAKROVA VLVI VROGRSCOMUNVA VLVI VROGRAKROVA VLVI KARAKROVA VLVI KARAKRO	140	SULDRD-PNSATOSIGSPLSHSDYST PV-E ILPTLYLGCAKUSINLDVI EEFGFKYYII NVIP	0 40
KI M. SHHIDAYI SHIMI SLADOYI SHIRVRI DENT SHIRVRI DENT CHRYKI DENT CHRYKI DENT CHRYKI DENT CHROT GHEDILL VIDF GHEDILL	150	AKOS I M. DVI AKOS I M. DVI AKADS I M. DVI	50
III VKHKKSHI III VKHKKSHI III VKHKKSHI III VKHRRSII II VKHRRSII EI VKHRRSII EI VKHRRSII EI VKHRRSHI SIVRHRE-II III VRHRRSCHI III VRHRRSCHI II VRHRRSCHI	160	Bic lun SKNKAHTI SA BH HILLI HA BH HILLI BH HA BH HILLI BH HA BH H	
IVKHEKSHISTWENI NGOLLINI VKEKKSHISTWENI NGOLLINI VKERKSHISTWENI NGOLLINI VKERREVISTWESI NGOLLOFI VKERRESIISTWESI NGOLLOFI VKERRSHISTWESI NGOLLOFI VKERRSHISTWESI NGOLLOFI VKERRSHISTWESI NGOLLOFI IVRORRSHISTWESTWEST NGOLLOFI IVRORRSCONUWOGET QROLDEFI IVRORRSCONUWOGE PROLITATION		I NV IP	70
LIFT RTL 63 SS I IFT RTL 63 SS I IFT RTL GL SS I YER H KIL IN LOFE SQVL IN H LOFE SQVL IN H LOYE SETLINST IN H CQLRURLICKES QEFEKNEVIIQYRQ L# #		NLTHLFENNG SCPKP-DF1C SCPNIIFE-G NCPNIIFE-G NCPNIIFE-G RISERCH-T HIMBHFYKDS	80
X X X X X X X X X X X X X X X X X X X	100183	AL FENNGEFKYKO IP 15MINISONI. SI AL FENNGEF IYKO IP 15MINISONI. SI AL FENNGEF I YKO IP 15MINISONI. SI AL FENNGEF I YKO IP 15MINISONI. SI ANTE GILTHYKSI PVENNIKINI I SI ANTE GHYQYKO IP VENSHITINI I SI ANTE THLHYKHI PVENSHITINI I SI SORPHLEGVKYLO IP ONDSPS IK SORPHLEGVKYLO IP ONDSPS IK SORPHLEGVKYLO IP ONDSPS IK	90
		DHIRSON SO DHIRSON SO DHIRSON SO DHIRSON SO DHIRSON SO DEFEN SO DE	, 10

DSP-3

Northern blot analysis



He = Heart

Br = Brain

Pl = Placenta Lu = Lung

Li = Liver

SM = Skeletal Muscle

• Ki = Kidney

Pa = Pancreas

FIGURE 4

muDSP3 cDNA

Figure 5

muDSP3 amino acids

MGSGMSQILPGLYIGNFKDARDAEQLSRNKVTHILSVHDTARPMLEGVKYLCIPAADTP SQNLTRHFKESIKFIHECRLQGES**CLVHCLAGVSRSVTLVIAYIM**TVTDFGWEDALHTV RAGRSCANPNLGFQRQLQEFEKHEVHQYRQWLREEYGENPLRDAEEAKNILGKYKEQGR MEPRPSSRRWSSFSTLPPLTYNNYTTET*

Figure 6